

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/016,869A

RECEIVED 1644

DATE: 06/15/2000
TIME: 06:10:00

INPUT SET: S35635.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Beach, David H.
Demetrick, Douglas J.
Serrano, Manuel
Hannon, Gregory J.

(ii) TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and
Uses Related Thereto

(iii) NUMBER OF SEQUENCES: 34

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Foley, Hoag & Eliot
(B) STREET: One Post Office Square
(C) CITY: Boston
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02109

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WordPad

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/016,869
(B) FILING DATE: 30-JAN-1998

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/893,274
(B) FILING DATE: 15-JUL-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/306,511
(B) FILING DATE: 14-SEP-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/248,812
(B) FILING DATE: 25-MAY-1994

(vii) PRIOR APPLICATION DATA:

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47 (A) APPLICATION NUMBER: US 08/227,371
48 (B) FILING DATE: 14-APR-1994
49
50 (vii) PRIOR APPLICATION DATA:
51 (A) APPLICATION NUMBER: US 08/154,915
52 (B) FILING DATE: 18-NOV-1993
53
54 (vii) PRIOR APPLICATION DATA:
55 (A) APPLICATION NUMBER: US 07/991,997
56 (B) FILING DATE: 17-DEC-1992
57
58 (viii) ATTORNEY/AGENT INFORMATION:
59 (A) NAME: Vincent, Matthew P.
60 (B) REGISTRATION NUMBER: 36,709
61 (C) REFERENCE/DOCKET NUMBER: MIV-071.10
62
63 (ix) TELECOMMUNICATION INFORMATION:
64 (A) TELEPHONE: (617) 832-1299
65 (B) TELEFAX: (617) 832-7000
66
67
68 (2) INFORMATION FOR SEQ ID NO:1:
69 (i) SEQUENCE CHARACTERISTICS:
70 (A) LENGTH: 994 base pairs
71 (B) TYPE: nucleic acid
72 (C) STRANDEDNESS: both
73 (D) TOPOLOGY: linear
74
75 (ii) MOLECULE TYPE: cDNA
76 (ix) FEATURE:
77 (A) NAME/KEY: CDS
78 (B) LOCATION: 41..508
79
80 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
81
82 CGGAGAGGGG GAGAACAGAC AACGGGCGGC GGGAGCAGC ATG GAT CCG GCG GCG 55
83 Met Asp Pro Ala Ala 5
84 1 5
85 GGG AGC AGC ATG GAG CCT TCG GCT GAC TGG CTG GCC ACG GCC GCG GCC 103
86 Gly Ser Ser Met Glu Pro Ser Ala Asp Trp Leu Ala Thr Ala Ala Ala
87 10 15 20
88 CGG GGT CGG GTA GAG GAG GTG CGG GCG CTG CTG GAG GCG GTG GCG CTG 151
89 Arg Gly Arg Val Glu Glu Val Arg Ala Leu Leu Glu Ala Val Ala Leu
90 25 30 35
91 CCC AAC GCA CCG AAT AGT TAC GGT CGG AGG CCG ATC CAG GTC ATG ATG 199
92 Pro Asn Ala Pro Asn Ser Tyr Gly Arg Arg Pro Ile Gln Val Met Met
93 40 45 50
94 ATG GGC AGC GCC CGA GTG GCG GAG CTG CTG CTG CTC CAC GGC GCG GAG 247
95 Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu His Gly Ala Glu
96 55 60 65
97 CCC AAC TGC GCC GAC CCC GCC ACT CTC ACC CGA CCC GTG CAC GAC GCT 295
98 Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val His Asp Ala
99 70 75 80 85

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100 GCC CGG GAG GGC TTC CTG GAC ACG CTG GTG GTG CTG CAC CGG GCC GGG      343
101 Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg Ala Gly
102                               90                               100
103 GCG CGG CTG GAC GTG CGC GAT GCC TGG GGC CGT CTG CCC GTG GAC CTG      391
104 Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp Leu
105                               105                               110
106 GCT GAG GAG CTG GGC CAT CGC GAT GTC GCA CGG TAC CTG CGC GCG GCT      439
107 Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg Tyr Leu Arg Ala Ala
108                               120                               130
109 GCG GGG GGC ACC AGA GGC AGT AAC CAT GCC CGC ATA GAT GCC GCG GAA      487
110 Ala Gly Gly Thr Arg Gly Ser Asn His Ala Arg Ile Asp Ala Ala Glu
111                               135                               145
112 GGT CCC TCA GAC ATC CCC GAT TGAAGAACC AGAGAGGCTC TGAGAAACCT      538
113 Gly Pro Ser Asp Ile Pro Asp
114                               150                               155
115 CGGGAAACTT AGATCATCAG TCACCGAAGG TCCTACAGGG CCACAACTGC CCCC GCCACA      598
116 ACCCACCCTG CTTTCGTAGT TTTTCATTAG AAAATAGAGC TTTTAAAAAT GTCCCTGCCTT      658
117 TTAACGTAGA TATAAGCCTT CCCCACCTAC CGTAAATGTC CATTATATC ATTTTATTATA      718
118 TATTCCTATA AAAATGTAAA AAAGAAAAAC ACCGCTTCTG CTTTTCCTCT GTGTTGGAGT      778
119 TTTCTGGAGT GAGCACTCAC GCCCTAAGCG CACATTCATG TGGGCATTTC TTGCGAGCCT      838
120 CGCAGCTTCC GGAAGCTGTC GACTTCATGA CAAGCATTTT GTGAAGTAGG GAAGCTCAGG      898
121 GGGGTACTCG GCTTCTCTTG AGTCACACTG CTAGCAAAATG GCAGAACCAA AGCTCAAATA      958
122 AAAATAAAAT TATTTTCATT CATTCACTCA AAAAAA      994

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

135 Met Asp Pro Ala Ala Gly Ser Ser Met Glu Pro Ser Ala Asp Trp Leu
136   1           5           10           15
137 Ala Thr Ala Ala Ala Arg Gly Arg Val Glu Glu Val Arg Ala Leu Leu
138           20           25           30
139 Glu Ala Val Ala Leu Pro Asn Ala Pro Asn Ser Tyr Gly Arg Arg Pro
140           35           40           45
141 Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu
142           50           55           60
143 Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg
144           65           70           75           80
145 Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val
146           85           90           95
147 Leu His Arg Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg
148           100          105          110
149 Leu Pro Val Asp Leu Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg
150           115          120          125
151 Tyr Leu Arg Ala Ala Ala Gly Gly Thr Arg Gly Ser Asn His Ala Arg
152           130          135          140

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153 Ile Asp Ala Ala Glu Gly Pro Ser Asp Ile Pro Asp
154 145 150 155
155
156 (2) INFORMATION FOR SEQ ID NO:3:
157
158 (i) SEQUENCE CHARACTERISTICS:
159 (A) LENGTH: 837 base pairs
160 (B) TYPE: nucleic acid
161 (C) STRANDEDNESS: single
162 (D) TOPOLOGY: linear
163 (ii) MOLECULE TYPE: cDNA
164
165 (ix) FEATURE:
166 (A) NAME/KEY: CDS
167 (B) LOCATION: 328..738
168
169 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
170
171 GAGGACTCCG CGACGGTCCG CACCCTGCGG CCAGAGCGGC TTGAGCTCG GCTGCTTCCG 60
172 CGCTAGCGCG TTTTCCAG AAGCAATCCA GCGCGCGCCG CTGGTCTTG AGCGCCAGGA 120
173 AAAGCCCGGA GCTAACGACC GGCCGCTCGG CACTGCACGG GCGCCCAAGC CGCAGAAGAA 180
174 GACGACCGGG AGGGTAATGA AGCTGAGCCC AGGTCTCCTA GGAAGGAGAG AGTGCGCCGG 240
175 AGCAGCGTGG GAAAGAAGGG AAGAGTGTCC TTAAGTTTAC GCCTAACGGT GGATTATCCG 300
176 GGCCGCTGCG CCGTCTGGGGG CTGCGGA ATG CGC GAG GAG AAC AAG GGC ATG 351
177 Met Arg Glu Glu Asn Lys Gly Met
178 1 5
179 CCC AGT GGG GGC GGC AGC GAT GAG GGT CTG GCC ACG CCG GCG CGG GGA 399
180 Pro Ser Gly Gly Gly Ser Asp Glu Gly Leu Ala Thr Pro Ala Arg Gly
181 10 15 20
182 CTA GTG GAG AAG GTG CGA CAC TCC TGG GAA GCC GGC GCG GAT CCC AAC 447
183 Leu Val Glu Lys Val Arg His Ser Trp Glu Ala Gly Ala Asp Pro Asn
184 25 30 35 40
185 GGA GTC AAC CGT TTC GGG AGG CGC GCG ATC CAG GTC ATG ATG ATG GGC 495
186 Gly Val Asn Arg Phe Gly Arg Arg Ala Ile Gln Val Met Met Met Gly
187 45 50 55
188 AGC GCC CGC GTG GCG GAG CTG CTG CTG CTC CAC GGC GCG GAG CCC AAC 543
189 Ser Ala Arg Val Ala Glu Leu Leu Leu Leu His Gly Ala Glu Pro Asn
190 60 65 70
191 TGC GCA GAC CCT GCC ACT CTC ACC CGA CCG GTG CAT GAT GCT GCC CGG 591
192 Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val His Asp Ala Ala Arg
193 75 80 85
194 GAG GGC TTC CTG GAC ACG CTG GTG GTG CTG CAC CGG GCC GGG GCG CGG 639
195 Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg Ala Gly Ala Arg
196 90 95 100
197 CTG GAC GTG CGC GAT GCC TGG GGT CGT CTG CCC GTG GAC TTG GCC GAG 687
198 Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp Leu Ala Glu
199 105 110 115 120
200 GAG CGG GGC CAC CGC GAC GTT GCA GGG TAC CTG CGC ACA GCC ACG GGG 735
201 Glu Arg Gly His Arg Asp Val Ala Gly Tyr Leu Arg Thr Ala Thr Gly
202 125 130 135
203 GAC TGACGCCAGG TTCCCCAGCC GCCACAACG ACTTTATTTT CTTACCCAAT 788
204 Asp
205

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206 TTCCCACCCC CACCCACCTA ATTCGATGAA GGCTGCCAAC GGGGAGCGG
207
208 (2) INFORMATION FOR SEQ ID NO:4:
209
210 (i) SEQUENCE CHARACTERISTICS:
211 (A) LENGTH: 137 amino acids
212 (B) TYPE: amino acid
213 (D) TOPOLOGY: linear
214
215 (ii) MOLECULE TYPE: protein
216
217 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
218
219 Met Arg Glu Glu Asn Lys Gly Met Pro Ser Gly Gly Gly Ser Asp Glu
220 1 5 10 15
221 Gly Leu Ala Thr Pro Ala Arg Gly Leu Val Glu Lys Val Arg His Ser
222 20 25 30
223 Trp Glu Ala Gly Ala Asp Pro Asn Gly Val Asn Arg Phe Gly Arg Arg
224 35 40 45
225 Ala Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu
226 50 55 60
227 Leu Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr
228 65 70 75 80
229 Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val
230 85 90 95
231 Val Leu His Arg Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly
232 100 105 110
233 Arg Leu Pro Val Asp Leu Ala Glu Glu Arg Gly His Arg Asp Val Ala
234 115 120 125
235 Gly Tyr Leu Arg Thr Ala Thr Gly Asp
236 130 135
237
238 (2) INFORMATION FOR SEQ ID NO:5:
239
240 (i) SEQUENCE CHARACTERISTICS:
241 (A) LENGTH: 853 base pairs
242 (B) TYPE: nucleic acid
243 (C) STRANDEDNESS: both
244 (D) TOPOLOGY: linear
245
246 (ii) MOLECULE TYPE: cDNA
247
248 (ix) FEATURE:
249 (A) NAME/KEY: CDS
250 (B) LOCATION: 213..587
251
252 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
253
254 GGAGTACAGC AGCGGGAGCA TGGGTCGCAG GTTCTTGATC ACTGTAAGGA TTCAGCGCGC 60
255
256 GGGCCGCCCA CTCCAAGAGA GGGTTTTCTT GGTGAAGTTC GTGCATATCC GGAGACCCAG 120
257
258 GACAGCGAGC TGCCTCTGG CTTCGTGAA CATGTTGTTG AGGCTAGAGA GGATCTTGAG 180

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SEQUENCE VERIFICATION REPORT
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Original Text